RAW SEQUENCE LISTING

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Application Serial Number: 08/765,108
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/765,108*

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:
(i) APPLICANT: Massachusetts Institute of Technology
(ii) TITLE OF INVENTION: Class BI and CI Scavenger Receptors
(iii) NUMBER OF SEQUENCES: 8
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30309-3450
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/765,108
(B) FILING DATE: 27-MAR-1997
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US95/07721
(B) FILING DATE: 19-JUN-1995
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: MIT6620
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (404) 873-8794
(B) TELEFAX: (404) 873-8795
(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ashkenas, et al.
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 34

(F) PAGES: 983-1000
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATGAAGAAC TGCTTAGTTT 20

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ashkenas, et al.
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 34
(F) PAGES: 983-1000
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATCAAGGAA TTTAACTG 18

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 156..1683
(D) OTHER INFORMATION: /function= "Nucleotides 156 through 1683 encode the amino acid sequence for the Hamster Scavenger Receptor Class B-I."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCACCTGCA GGGCTACTGC TGCTCCGGCC ACTGCCTGAG ACTCACCTTG CTGGAACGTG 60

AGCCTCGGCT TCTGTCATCT CTGTGGCCTC TGTCGCTTCT GTCGCTGTCC CCCTTCAGTC 120

CCTGAGCCCC GCGAGCCCGG GCCGCACACG CGGACATGGG CGGCAGCGCC AGGGCGCGCT 180

GGGTGGCGGT GGGGCTGGGC GTCGTGGGGC TGCTGTGCGC TGTGCTCGGT GTGGTTATGA 240

TCCTCGTGAT GCCCTCGCTC ATCAAACAGC AGGTACTGAA GAATGTCCGC ATAGACCCCA 300

GCAGCCTGTC CTTTGCAATG TGGAAGGAGA TCCCTGTACC CTTCTACTTG TCCGTCTACT 360

TCTTCGAGGT GGTCAATCCC AGCGAGATCC TAAAGGGTGA GAAGCCAGTA GTGCGGGAGC 420

GTGGACCCTA TGTCTACAGG GAATTCAGAC ATAAGGCCAA CATCACCTTC AATGACAATG 480

ATACTGTGTC CTTTGTGGAG CACCGCAGCC TCCATTTCCA GCCGGACAGG TCCCACGGCT 540

CTGAGAGTGA CTACATTATA CTGCCTAACA TTCTGGTCTT GGGGGGCGCA GTAATGATGG 600

AGAGCAAGTC TGCAGGCCTG AAGCTGATGA TGACCTTGGG GCTGGCCACC TTGGGCCAGC 660

GTGCCTTTAT GAACCGAACA GTTGGTGAGA TCCTGTGGGG CTATGAGGAT CCCTTCGTGA 720

ATTTTATCAA CAAATACTTA CCAGACATGT TCCCCATCAA GGGCAAGTTC GGCCTGTTTG 780

TTGAGATGAA CAACTCAGAC TCTGGGCTCT TCACTGTGTT CACGGGCGTC CAGAACTTCA 840

GCAAGATCCA CCTGGTGGAC AGATGGAATG GGCTCAGCAA GGTCAACTAC TGGCATTCAG 900

AGCAGTGCAA CATGATCAAT GGCACTTCCG GGCAGATGTG GGCACCATTC ATGACACCCC 960

AGTCCTCGCT GGAATTCTTC AGTCCGGAAG CCTGCAGGTC TATGAAGCTC ACCTACCATG 1020

ATTCAGGGGT GTTTGAAGGC ATCCCCACCT ATCGCTTCAC AGCCCCTAAA ACTTTGTTTG 1080

CCAATGGGTC TGTTTACCCA CCCAATGAAG GTTTCTGCCC GTGCCTTGAA TCCGGCATTC 1140

AAAATGTCAG CACTTGCAGG TTTGGTGCAC CCCTGTTTCT GTCACACCCT CACTTCTACA 1200

ATGCAGACCC TGTGCTATCA GAAGCCGTTC TGGGTCTGAA CCCTGACCCA AGGGAGCATT 1260

CTTTGTTCCT TGACATCCAT CCGGTCACTG GGATCCCCAT GAACTGTTCT GTGAAGTTGC 1320

AGATAAGCCT CTACATCAAA GCTGTCAAGG GCATTGGGCA AACAGGGAAG ATCGAGCCCG 1380

TGGTCCTCCC ATTGCTGTGG TTTGAGCAGA GCGGTGCCAT GGGCGGCGAG CCCCTGAACA 1440

CGTTCTACAC GCAGCTGGTG CTGATGCCCC AGGTACTTCA GTATGTGCAG TATGTGCTGC 1500

TGGGGCTGGG CGGCCTCCTG CTGCTGGTGC CCGTCATCTA CCAGTTGCGC AGCCAGGAGA 1560

AATGCTTTTT ATTTTGGAGT GGTAGTAAAA AGGGCTCGCA GGATAAGGAG GCCATTCAGG 1620

CCTACTCTGA GTCTCTGATG TCACCAGCTG CCAAGGGCAC GGTGCTGCAA GAAGCCAAGC 1680

TGTAGGGTCC CAAAGACACC ACGAGCCCCC CCAACCTGAT AGCTTGGTCA GACCAGCCAT 1740

CCAGCCCCTA CACCCCGCTT CTTGAGGACT CTCTCAGCGG ACAGTCGC 1788

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..509
(D) OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger Receptor Class B-I."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 9..32
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 440..464
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..385
(D) OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175, 212-214, 227-229, 255-257,310-312, 330-332 and 383-385 represent potential N-linked glycosylation sites."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21..470
(D) OTHER INFORMATION: /note= "The cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide linkages."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Gly Gly Ser Ala Arg Ala Arg Trp Val Ala Val Gly Leu Gly Val
1               5                  10                  15

Val Gly Leu Leu Cys Ala Val Leu Gly Val Val Met Ile Leu Val Met
            20                  25                  30

Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro
        35                  40                  45

Ser Ser Leu Ser Phe Ala Met Trp Lys Glu Ile Pro Val Pro Phe Tyr
    50                  55                  60

Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Ser Glu Ile Leu Lys
65                  70                  75                  80
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206
207       Gly Glu Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu
208                       85                  90                  95
209
210       Phe Arg His Lys Ala Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser
211                   100                 105                 110
212
213       Phe Val Glu His Arg Ser Leu His Phe Gln Pro Asp Arg Ser His Gly
214               115                 120                 125
215
216       Ser Glu Ser Asp Tyr Ile Ile Leu Pro Asn Ile Leu Val Leu Gly Gly
217           130                 135                 140
218
219       Ala Val Met Met Glu Ser Lys Ser Ala Gly Leu Lys Leu Met Met Thr
220       145                 150                 155                 160
221
222       Leu Gly Leu Ala Thr Leu Gly Gln Arg Ala Phe Met Asn Arg Thr Val
223                       165                 170                 175
224
225       Gly Glu Ile Leu Trp Gly Tyr Glu Asp Pro Phe Val Asn Phe Ile Asn
226                   180                 185                 190
227
228       Lys Tyr Leu Pro Asp Met Phe Pro Ile Lys Gly Lys Phe Gly Leu Phe
229               195                 200                 205
230
231       Val Glu Met Asn Asn Ser Asp Ser Gly Leu Phe Thr Val Phe Thr Gly
232           210                 215                 220
233
234       Val Gln Asn Phe Ser Lys Ile His Leu Val Asp Arg Trp Asn Gly Leu
235       225                 230                 235                 240
236
237       Ser Lys Val Asn Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly
238                       245                 250                 255
239
240       Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Gln Ser Ser Leu
241                   260                 265                 270
242
243       Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr His
244               275                 280                 285
245
246       Asp Ser Gly Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
247           290                 295                 300
248
249       Lys Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
250       305                 310                 315                 320
251
252       Cys Pro Cys Leu Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
253                       325                 330                 335
254
255       Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
256                   340                 345                 350
257
258       Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asp Pro Arg Glu His
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/765,108*

DATE: 02/17/2006
TIME: 13:00:43

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